

OIKE

RAW SEQUENCE LISTING

DATE: 12/21/2001

PATENT APPLICATION: US/09/830,123

TIME: 12:47:50

Input Set : A:\001560-397.ST25.txt

Output Set: N:\CRF3\12212001\I830123.raw

**Does Not Comply
Corrected Diskette Needed**

4 <110> APPLICANT: Iida, Shigeru
 5 Tanaka, Sachiko
 6 Inagaki, Yoshishige
 8 <120> TITLE OF INVENTION: Genes Encoding Proteins Regulating the pH of Vacuoles
 10 <130> FILE REFERENCE: 001560-397
 12 <140> CURRENT APPLICATION NUMBER: 09/830,123
 13 <141> CURRENT FILING DATE: 2001-04-24
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP00/05722
 16 <151> PRIOR FILING DATE: 2000-08-24
 18 <150> PRIOR APPLICATION NUMBER: JP 11/236800
 19 <151> PRIOR FILING DATE: 1999-08-24
 21 <160> NUMBER OF SEQ ID NOS: 20
 23 <170> SOFTWARE: PatentIn version 3.1

ERRORED SEQUENCES

196 <210> SEQ ID NO: 2
 197 <211> LENGTH: 542
 198 <212> TYPE: PRT
 199 <213> ORGANISM: Ipomea nil
 201 <220> FEATURE:
 202 <221> NAME/KEY: peptide
 203 <222> LOCATION: (1)..(542)
 204 <223> OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
 207 <400> SEQUENCE: 2
 209 Met Ala Phe Gly Leu Ser Ser Leu Leu Gln Asn Ser Asp Leu Phe Thr
 210 1 5 10 15
 212 Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
 213 20 25 30
 215 Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
 216 35 40 45
 218 Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
 219 50 55 60
 221 Ile Leu Leu Leu Ser Gly Lys Ser Ser His Leu Leu Val Phe Ser
 222 65 70 75 80
 224 Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
 225 85 90 95
 227 Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile
 228 100 105 110
 230 Met Leu Phe Gly Ala Ile Gly Thr Leu Ile Ser Cys Ser Ile Ile Ser
 231 115 120 125
 233 Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp
 234 130 135 140
 236 Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser
 237 145 150 155 160
 239 Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr

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240                               165                               170                               175
242 Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val Val
243                               180                               185                               190
245 Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys
246                               195                               200                               205
248 Ile Gly Leu His Phe Ile Gly Asn Phe Leu Tyr Leu Phe Leu Ser Ser
249                               210                               215                               220
251 Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys
252 225                               230                               235                               240
254 Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met
255                               245                               250                               255
257 Met Leu Met Ser Tyr Leu Ser Tyr Ile Met Ala Glu Leu Phe Tyr Leu
258                               260                               265                               270
260 Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr
261                               275                               280                               285
263 Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Arg His Ser
E--> 264 290                               295                               300 300
266 Phe Ala Thr Leu Ser Phe Val Ala Glu Thr Phe Ile Phe Leu Tyr Val
267 305                               310                               315                               320
269 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser
270                               325                               330                               335
272 Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu
273                               340                               345                               350
275 Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
276                               355                               360                               365
278 Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile
279 370                               375                               380
281 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
282 385                               390                               395                               400
284 Tyr Asn Lys Phe Thr Ser Gly His Thr Ser Leu His Glu Asn Ala
285                               405                               410                               415
287 Ile Met Ile Thr Ser Thr Val Thr Val Val Leu Phe Ser Thr Val Val
288                               420                               425                               430
290 Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Leu Pro Pro His
291                               435                               440                               445
293 Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser
294 450                               455                               460
296 Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser
297 465                               470                               475                               480
299 Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu
300                               485                               490                               495
302 Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg
303                               500                               505                               510
305 Lys Phe Asp Asp Ser Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe
306                               515                               520                               525
308 Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
309 530                               535                               540
938 <210> SEQ ID NO: 17
939 <211> LENGTH: 553

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940 <212> TYPE: PRT
941 <213> ORGANISM: Nierembergia hybrida
943 <220> FEATURE:
944 <221> NAME/KEY: peptide
945 <222> LOCATION: (1)..(553)
946 <223> OTHER INFORMATION: Amino acid sequence of protein regulating the pH of vacuoles
948 <400> SEQUENCE: 17
950 Met Ala Phe Asp Phe Gly Thr Leu Leu Gly Lys Met Asn Asn Leu Thr
951              5              10              15
953 Thr Ser Asp His Gln Ser Val Val Ser Val Asn Leu Phe Val Ala Leu
954              20              25              30
956 Ile Cys Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp
957              35              40              45
959 Met Asn Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Val
960              50              55              60
962 Ile Ile Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe
963 65              70              75              80
965 Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
966              85              90              95
968 Ala Gly Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr
969              100             105             110
971 Ile Met Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Ile Ile Ile
972              115             120             125
974 Ser Ala Gly Ala Ile Gly Ile Phe Lys Lys Met Asp Ile Gly His Leu
975              130             135             140
977 Glu Ile Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp
978 145             150             155             160
980 Ser Val Cys Thr Leu Gln Val Leu Asn Gln Glu Glu Thr Pro Leu Leu
981              165             170             175
984 Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
985              180             185             190
987 Val Leu Phe Asn Ala Val Gln Asn Phe Asp Leu Ser His Ile Ser Thr
988              195             200             205
990 Gly Lys Ala Leu Gln Leu Ile Gly Asn Phe Leu Tyr Leu Phe Ala Ser
991              210             215             220
993 Ser Thr Phe Leu Gly Val Ala Val Gly Leu Leu Ser Ala Phe Ile Ile
994 225             230             235             240
996 Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Ile
997              245             250             255
999 Met Ile Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Tyr
1000             260             265             270
1002 Leu Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His
1003             275             280             285
1005 Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His
1006             290             295             300
1008 Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Ile Phe Leu Tyr
1009 305             310             315             320
1011 Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp
1012             325             330             335

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```

1014 Ser Pro Gly Thr Ser Ile Lys Val Ser Ser Ile Leu Leu Gly Leu Val
1015          340          345          350
1017 Leu Val Gly Arg Gly Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn
1018          355          360          365
1020 Leu Thr Lys Lys Asn Pro Glu Asp Lys Ile Ser Phe Asn Gln Gln Val
1021          370          375          380
1023 Thr Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Met Ala Leu
1024 385          390          395          400
1026 Ala Tyr Asn Gln Phe Thr Arg Gly Gly His Thr Gln Leu Arg Ala Asn
1027          405          410          415
1029 Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val
1030          420          425          430
1032 Val Phe Gly Leu Met Thr Lys Pro Leu Ile Leu Leu Leu Leu Pro Ser
1033          435          440          445
1035 Gln Lys His Leu Ile Arg Met Ile Ser Ser Glu Pro Met Thr Pro Lys
1036          450          455          460
1038 Ser Phe Ile Val Pro Leu Leu Asp Ser Thr Gln Asp Ser Glu Ala Asp
E--> 1039 465          470->          475->          480->
1041 Leu Gly Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser
E--> 1042          485          490          495
1044 Thr Pro Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala
E--> 1045          500          505          510
1047 Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro
E--> 1048          515          520          525
1050 Gly Ser Pro Thr Glu Pro Val Glu Pro Thr Glu Pro Arg Pro Ala Glu
E--> 1051          530          535          540
1053 Ser Arg Pro Thr Glu Pro Thr Asp Glu
E--> 1054 545          550

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VERIFICATION SUMMARY

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Input Set : A:\001560-397.ST25.txt

Output Set: N:\CRF3\12212001\I830123.raw

L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:177 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:264 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:610 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:614 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:618 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:14
L:839 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:843 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:851 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:855 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:859 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:863 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:891 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:895 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:907 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16

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Input Set : A:\001560-397.ST25.txt

Output Set: N:\CRF3\12212001\I830123.raw

L:911 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:915 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:919 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:1039 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:1087 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:18